

1	11	21	31	41
ACACACCATA	TGTGCCCCGAG	CCAGCCGACC	TATCCGGGCG	ATCCCGGGCC
TGTGTGGTAT	ACACGGGCTC	GGTCGGCTGG	ATAGGCCCGC	TAGGGCCCCG
51	61	71	81	91
GGTGGAAGAT	CTGATCCGCT	TTTATGATAA	CCTGCAGCAG	TGGCTGAACT
CCACCTTCTA	GACTAGGCGA	AAATACTATT	GGACGTCGTC	ACCGACTTGA
101	111	121	131	
GCGTGACCGC	CGCCTGCTAG	GGATCCACAC	AC	
CGCACTGGCG	GCGGACGATC	CCTAGGTGTG	TG	

FIGURE 2

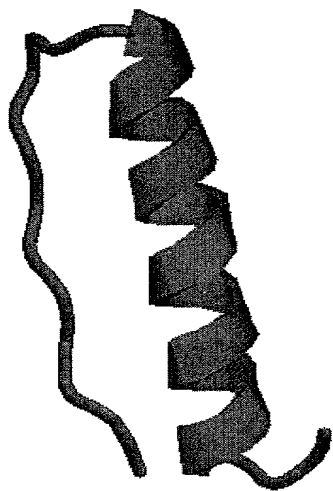


FIGURE 3

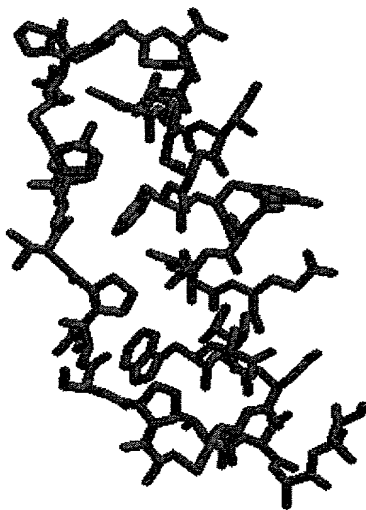


FIGURE 4

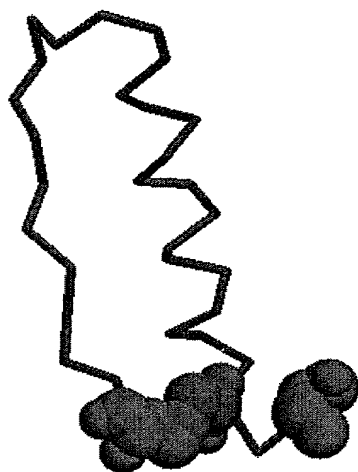


FIGURE 5

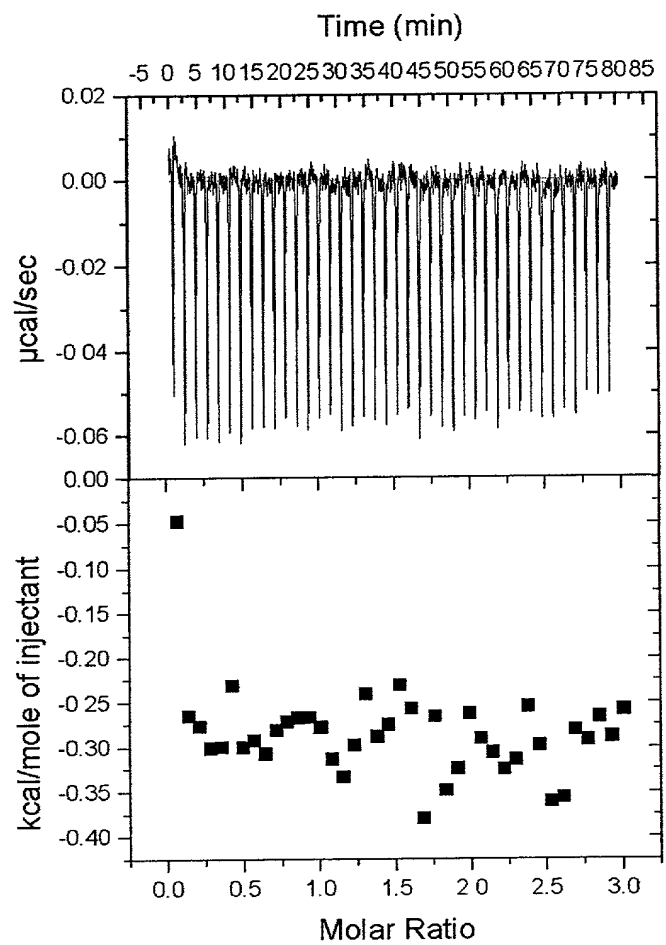


FIGURE 6

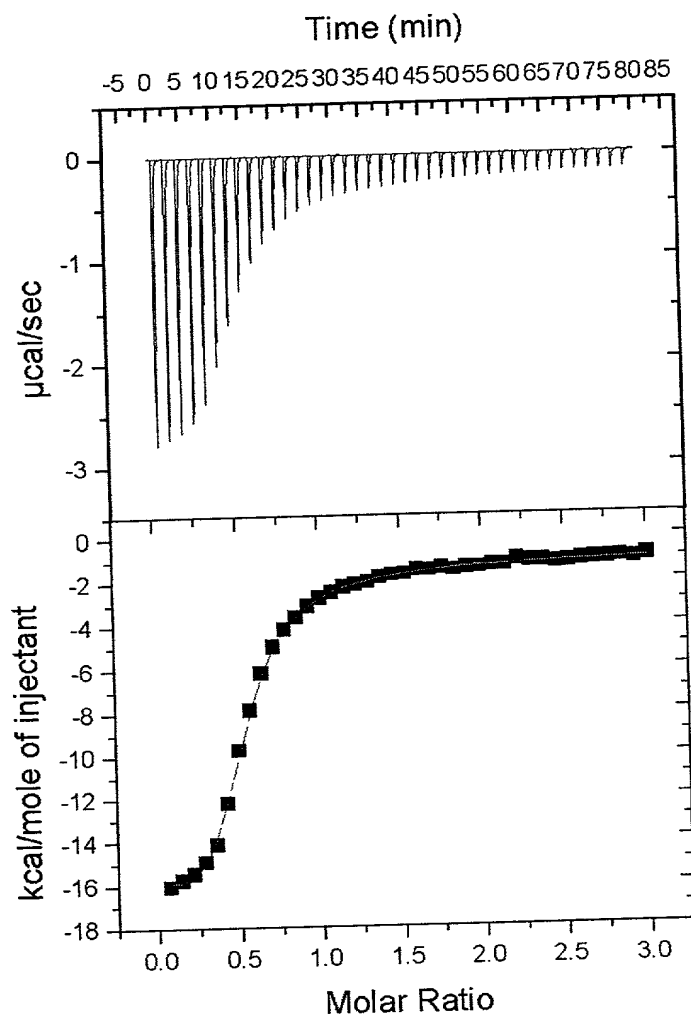


FIGURE 7

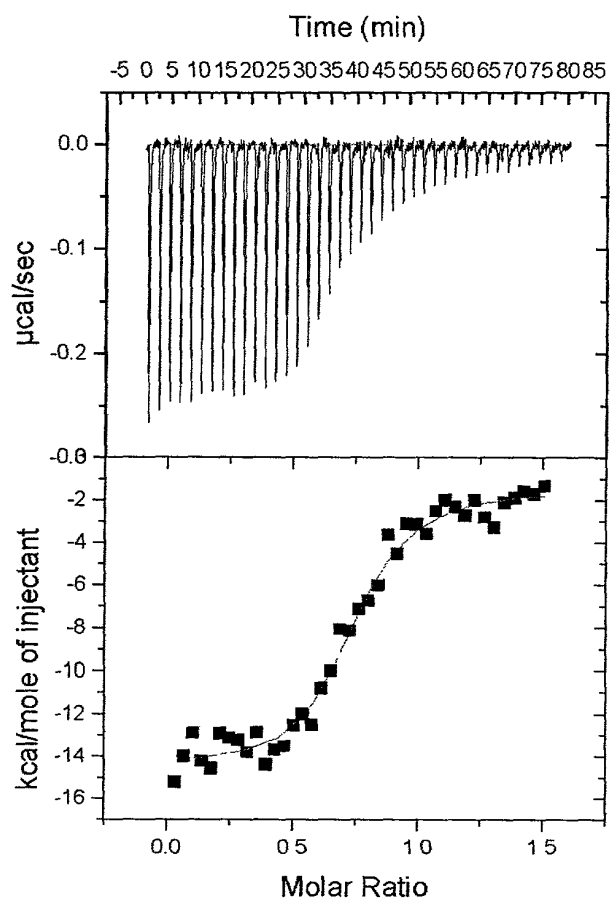


FIGURE 8

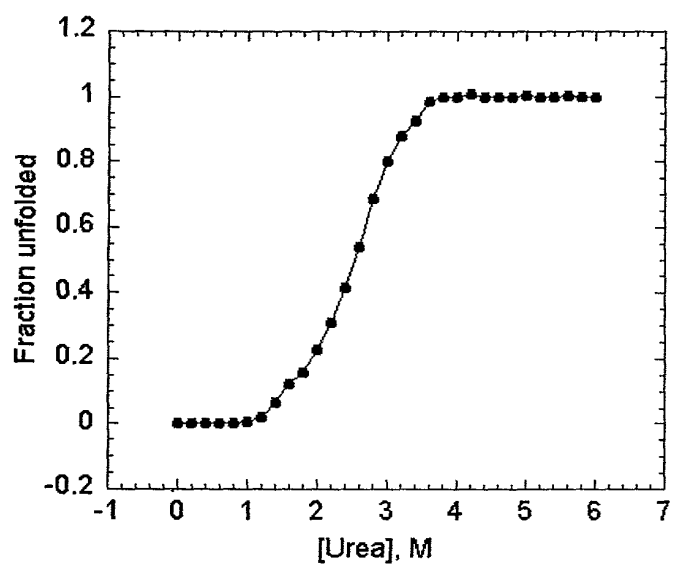


FIGURE 9

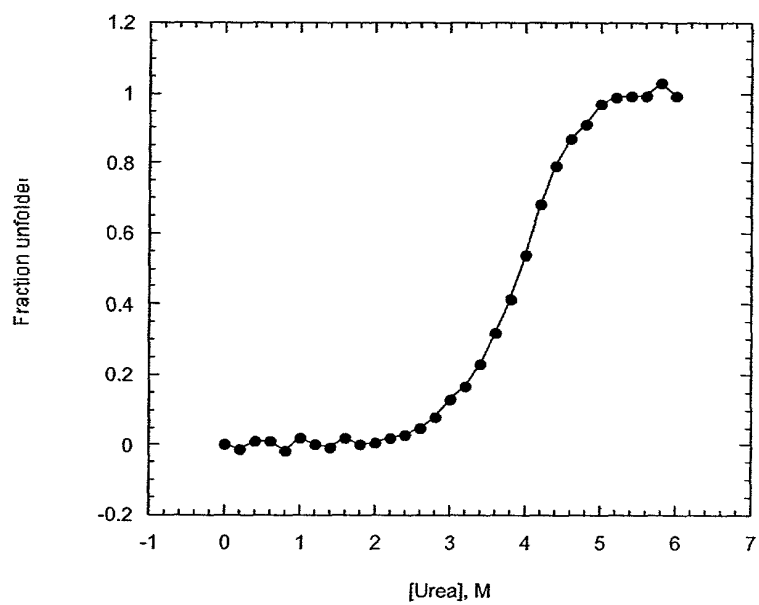


FIGURE 10

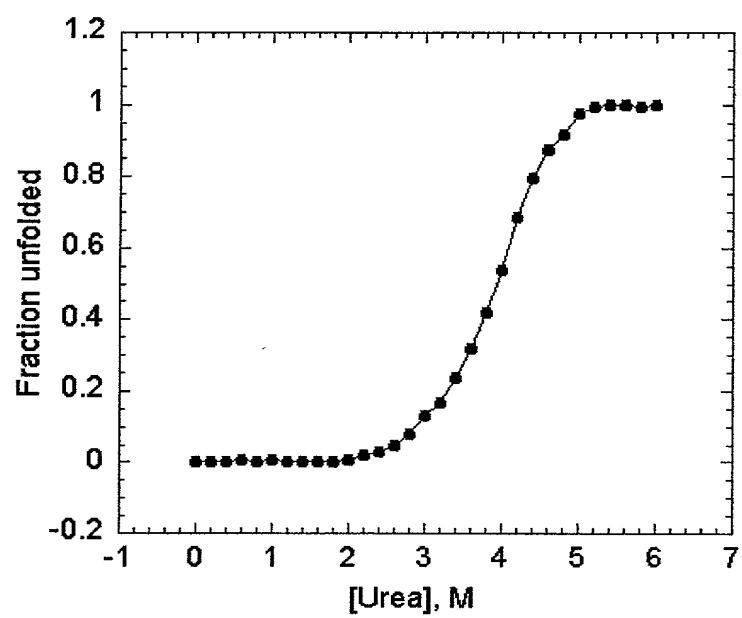


FIGURE 11

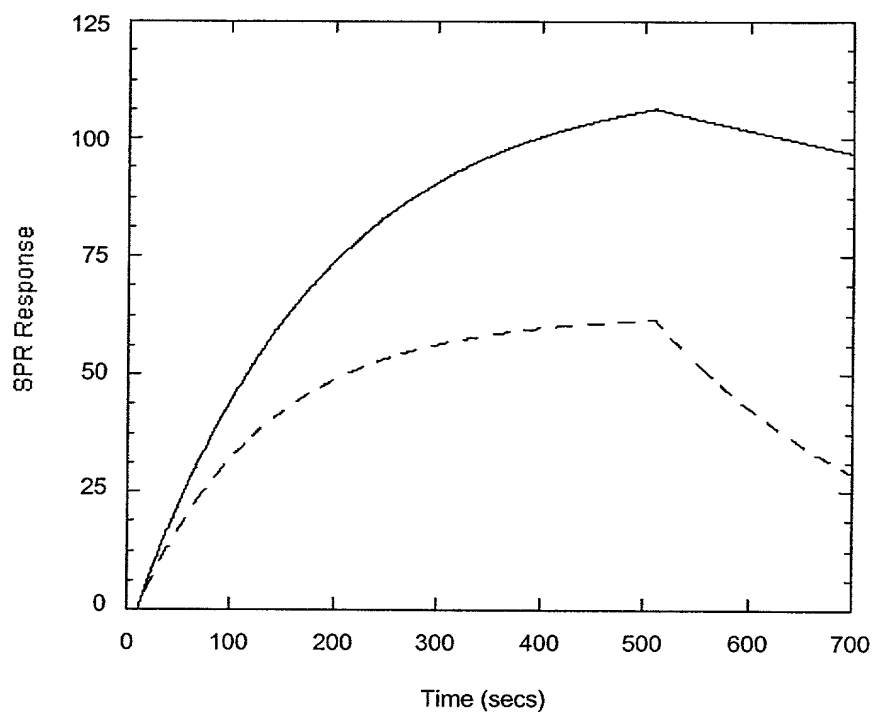


FIGURE 12

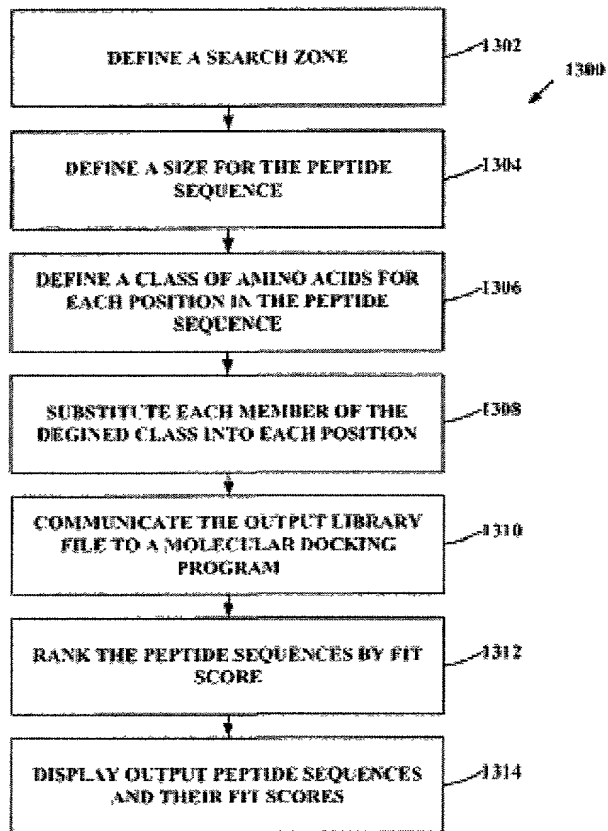


FIG. 13

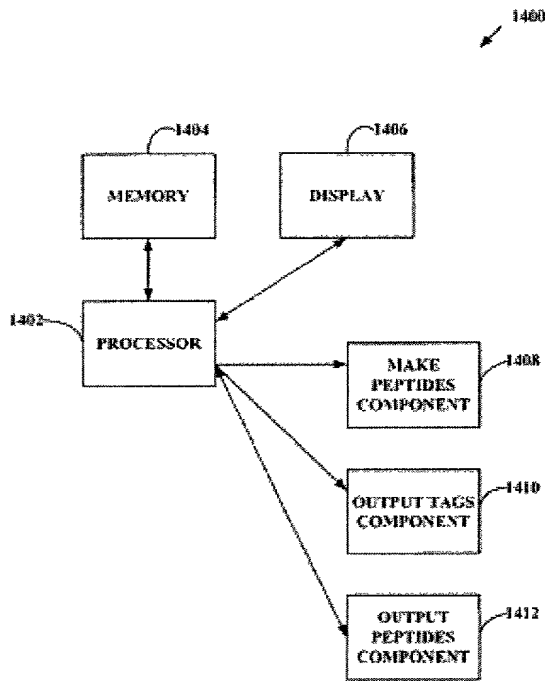


FIG. 14

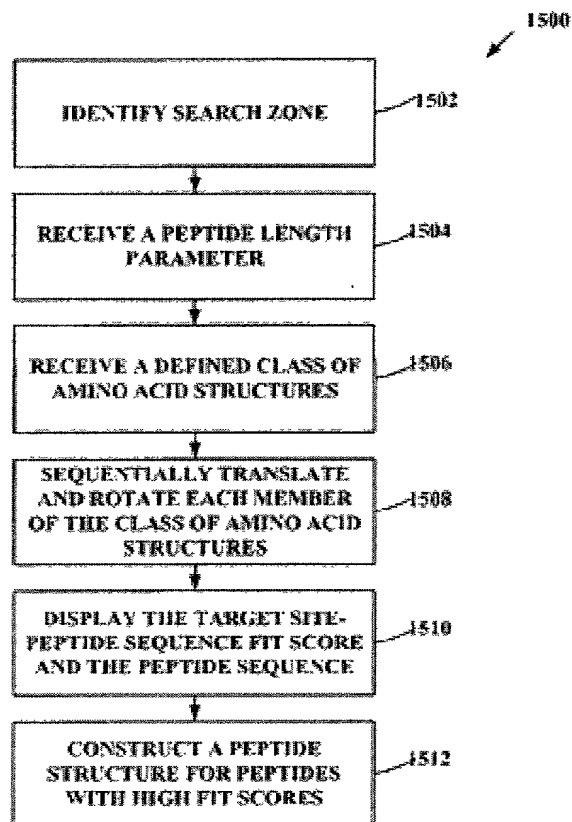


FIG. 15